

A:Molecule type: DNA
A:Residues: 1-509 <CHL>
C:Superfamily: glycinin

Query Match 33.4%; Score 118; DB 2; Length 509;
Best Local Similarity 37.0%; Pred. No. 4.6e-05;
Matches 34; Conservative 10; Mismatches 14; Indels 34; Gaps 5;

OY 3 DPQOREYEDCRRRCQOEPRQOYOCQORC-----REOQ-----ROH----- 38
|||:||||:| ||| ||| |||:| |||
Db 1 DPQRR-YEECCQOECHQOEPRQOPOCCQRC|KRFEDQEOQOSORQOFECQCHQOEORPK 59

OY 39 -----GKGGLINPORGSGRYEEGEKOS 63
| ||| | ||| |||:| |||
Db 60 KQOCVRECKRYQENPMWRC--FREEAEFEET 89

RESULT 3
FWCNAB
alpha-globulin B precursor (clone C72) - upland cotton

N:Alternate names: seed storage protein; vicilin precursor
C:Species: Gossypium hirsutum (upland cotton)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A30838; S06911

R:Chian, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986

A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII c
A:Reference number: A30838

A:Accession: A30838
A:Molecule type: mRNA

A:Residues: 1-588 <CHL>
A:Cross-references: GB:M16891; NID:g167374; PIDN:AAA3071.1; PID:g167375

A:Experimental source: var. Coker 201
R:Chian, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.

Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Se
A:Reference number: S06398

A:Accession: S06911
A:Status: not compared with conceptual translation

A:Molecule type: DNA
A:Residues: 1-81 <CH2>

C:Comment: This is a seed storage protein.
C:Superfamily: glycinin

C:Keywords: glycoprotein; seed; storage protein
F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-588/Product: alpha-globulin storage protein #status predicted <MAT>
F:411/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 31.2%; Score 110; DB 1; Length 588;
Best Local Similarity 33.3%; Pred. No. 0.00035;
Matches 33; Conservative 12; Mismatches 14; Indels 40; Gaps 6;

OY 3 DPQOREYEDCRRRCQOEPRQOYOCQORC-----REOQ-----ROHGGGLINPQ 48
|||:||||:| ||| ||| |||:| |||
Db 82 DPQRR-YEECCQOECHQOEPRQOPOCCQRC|KRFEDQEOQOSORQOFECQCHQOEORPK 139

OY 49 RGS-----GRY-----EEGEKOS 63
| ||| | ||| |||:| |||
Db 140 KQOCVRECKRYQENPMWRC--FREEAEFEETREGQEOS 178

RESULT 4
S35221
globulin Bgl precursor - barley

C:Species: Hordeum vulgare (barley)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

C:Accession: S35221
R:Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D.

Mol. Gen. Genet. 239, 209-218, 1993
A:Title: Barley embryo globulin 1 gene. Bgl1: characterization of cDNA, chromosome map
A:Reference number: S35221; MUID:93287988

A:Accession: S35221
A:Molecule type: mRNA
A:Residues: 1-637 <HEC>
A:Cross-references: EMBL:M64372; NID:g167003; PIDN:AAA2936.1; PID:g167004
C:Genetics:

A:Gene: Bgl1
A:Map position: 4
C:Superfamily: glycinin
C:Keywords: glycoprotein
F:174-190/Product: globulin Bgl1 #status predicted <MAT>

Query Match 29.2%; Score 103; DB 2; Length 637;
Best Local Similarity 31.9%; Pred. No. 0.002;
Matches 22; Conservative 11; Mismatches 20; Indels 16; Gaps 2;

OY 10 EDCRRRCQOEPRQOY-OCQRCREQORHGGGLINPQR-----GSG 53
| ||| | ||| | ||| | ||| |||:| |||
Db 42 QOCVRCQOEPRRYSHARCVCQCDQDQOHGRHEQEEQGRGWHGGEEREHGRGRG 101

OY 54 RYEEGEKO 62
| ||| | ||| |||:| |||
Db 102 RHGSEFREE 110

RESULT 5
S06398
alpha-globulin type A precursor - upland cotton

N:Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S06398

R:Chian, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987

A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A:Reference number: S06398

A:Accession: S06398
A:Status: not compared with conceptual translation

A:Molecule type: DNA
A:Residues: 1-605 <CHL>

C:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-605/Product: alpha-globulin type A #status predicted <MAT>

Query Match 28.8%; Score 101.5; DB 2; Length 605;
Best Local Similarity 33.3%; Pred. No. 0.0028;
Matches 20; Conservative 12; Mismatches 7; Indels 21; Gaps 2;

OY 3 DPQOREYEDCRRRCQOEPRQOYOCQORCQORHGGGLINPORGSGRYEEGEKO 62
|||:||||:| ||| | ||| | ||| |||:| |||
Db 79 DPQRR-YODCRHCCQOEPRRLRPNCQSCREQ-----YEQQQQQ 117

RESULT 6
T44430
protein PV100 [imported] - winter squash

C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44430

R:Yamada, K.; Shinada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, I.
J. Biol. Chem. 274, 2563-2570, 1999

A:Title: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a sin
A:Reference number: Z22767; MUID:99107919

A:Accession: T44430
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-810 <YAW>

A:Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062

Query Match 25.4%; Score 89.5; DB 2; Length 810;
Best Local Similarity 33.3%; Pred. No. 0.063;

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Matches 22; Conservative 15; Mismatches 24; Indels 5; Gaps 3;
QY      1  KNDPOORETEDCRRRCCEODE--PROOYCQCRRCRE--QORQHGRCGLINPORGSGRYE 56
      :  :  |||  |||  |||  :  |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      70  QNGSPRAEYEVCRILCOVAENGVCFOORRCCEQVCEERLRREREGRNGEDVDEVER--RDPPEWE 128
QY      57  EGGEKK 62
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      129  REEQR 134

RESULT 7
T01662
globalin-1 - maize (fragment)
C.Species: Zea mays (maize)
C.Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 11-Jan-2000
C.Accession: T01662
R.Hilton, H.; Gaut, B.S.
Genetics 150, 863-872, 1998
A.Title: Speciation and domestication in maize and its wild relatives: evidence from the
A.Reference number: 214386; MUID:98429537
A.Accession: T01662
A.Status: preliminary; translated from GR/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-236 <HIL>
A.Cross-references: EMBL:AF064222; NID:93414836; PIDN:AC031465.1; PID:93414837
A.Experimental source: subspecies parviglumis
C.Genetics:
A.Introns: 166/1; 224/3
C.Superfamily: glycinein

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Query Match	23.8%	Score 84	DB 2	Length 236
Best Local Similarity	35.0%	Pred. No. 0.08		
Matches	21	Conservative	6	Mismatches 19; Indels 14; Gaps 2
Oy	12	CRRREOQEPKROOYCCQRRCREQOQHGHGGDLINPQRCGSGRYE-----ECGEKQ	62	
Db	40	CVRREDRHWIOHPCRCLECCREERSRHEDD-----RSGESSSEDERRKOEKEKEKE	94	

RESULT 8
S25365
CYC8 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: glucose repression mediator; protein YBR0908; protein YBR112c; SSN6
C:Species: Saccharomyces cerevisiae
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000
A:Accession: S25365; S48277; S45980; S25404; S25405; A30906; S44692
R:Mannhaupt, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.
Yeast 8, 397-408, 1992
A:Title: Molecular analysis of yeast chromosome II between CND1 and LYS2: the excision
A:Reference number: S25364; MUID:92327848
A:Accession: S25365
A:Molecule type: DNA
A:Residues: 1-966 <MAN>
A:Cross-references: EMBL:X66247; NID:93548; PIDN:CAA6973.1; PID:93550
R:Mannhaupt, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A:Reference number: S48255; MUID:95208357
A:Accession: S48277
A:Status: nucleic acid sequence not shown: translation not shown
A:Molecule type: DNA
A:Residues: 1-966 <MAN>
A:Cross-references: EMBL:X78993; NID:9476045; PIDN:CAA55615.1; PID:9476068
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R:Feldmann, H.; Mannhaupt, G.; Schwarze, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45927
A:Accession: S45980
A:Molecule type: DNA
A:Residues: 1-966 <FE2>
A:Cross-references: EMBL:Z35981; NID:9536449; PIDN:CAA85069.1; PID:9536450; MIPS:YBR112d

R:Schultz, J., Carlson, M.
Mol. Cell. Biol. 7, 3637-3645, 1987
A:Title: Molecular analysis of SSN6, a gene functionally related to the SNF1 protein
A:Reference number: S25404; MUID:88065502
A:Accession: S25404
A:Molecule type: DNA
A:Residues: 1-546, 'K', 548-966 <SCH>
A:Cross-references: EMBL:M17826; NID:g172725; PIDN:AAA35103.1; PID:g172726
R:Trumbly, R.J.
Gene 73, 97-111, 1988
A:Title: Cloning and characterization of the CTC8 gene mediating glucose repression i
A:Reference number: S25405; MUID:89211964
A:Accession: S25405
A:Molecule type: DNA
A:Residues: 1-546, 'K', 548-966 <TRD>
A:Cross-references: EMBL:M23440; NID:g171349; PIDN:AAA34545.1; PID:g171350
C:Genetics:
A:Gene: SGD:CYC8; SSN6; CRT8
A:Cross-references: SGD:S0000316; MIPS:YBR112C
A:Map position: 2R
C:Function:
C:Description: required for complete derepression of IC14; required for repression of
C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
C:Keywords: nucleus; transcription regulation
F:224-257/Domain: tetratricopeptide repeat homology <TT1>
F:262-295/Domain: tetratricopeptide repeat homology <TT2>
F:296-329/Domain: tetratricopeptide repeat homology <TT3>
F:330-363/Domain: tetratricopeptide repeat homology <TT4>
F:365-398/Domain: tetratricopeptide repeat homology <TT5>

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Query Match Score 81 DB 2 Length 966.
Best Local Similarity 32.0% Pred No. 0.577
Matches 16; Conservative 16; Mismatches 18; Indels 0; Gaps 0.
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RESULT      9
T13398      gene mastermind protein - fruit fly (Drosophila virilis)
C:Species:   Drosophila virilis
C>Date:      20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
A:Accession: T13398
R:Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Evol. 38, 637-641, 1994
A>Title:      Drive-selection equilibrium: homopolymer evolution in the Drosophila gene ma
A:Reference number: Z17850; MUID:94365848
A:Accession: T13398
A>Status:     preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues:   1-1655 <NEW>
A:Cross-references: EMBL:M92914; NID:g157833; PID:g157834; PIDN:AAC37201.1


Query Match          22.2%; Score 78.5; DB 2; Length 1655;
Best Local Similarity 32.8%; Pred. No. 1.7;
Matches 19; Conservative 14; Mismatches 16; Indels 9; Gaps 1;


OY       5    QQREEDRCRRCCDEOEPRGYQCQRCEEROH-----GRGGDLINPORGSGG 53
            |||:::~::~|||:::||:::||::|||::|||::|||::|||::|||::|||::|||::|||
Db        379  QQQQHQHQHQHQDQHQQDQHQQDQHQQDQHNNHHQQDQDQGGLGLGNNGRGSGG 436


RESULT      10
T29475      hypothetical protein T01D1.6 - Caenorhabditis elegans
C:Species:    Caenorhabditis elegans
C>Date:       15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
A:Accession:  T29475
R:Bradshaw, H.; Wohlmann, P.
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